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Sheet	1	of	4

Complete if Known	
Application Number	09/827,960
Filing Date	April 4, 2001
First Named Inventor	MAYO, Stephen L.
Group Art Unit	1631
Examiner Name	
Attorney Docket Number	A-65353-7/RFT/RMS/RMK

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	A1	Brenner and Berry, A., et al., "A quantitative methodology for the de novo design of proteins", Protein Sci. 3:1871-1882 (Oct. 1994).	
	A2	Borman, "Proteins to Order," Chemical and Engineering Newsletter (C&EN) Oct. 6, 1997, 9-10 (1997).	
	A3	Bowie, J.U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions", Science vol.247:1306-1310 (Mar. 1990).	
	A4	Bowie, J.U., et al., "A Method to Identify Protein Sequences that Fold into a Known Three-Dimensional Structure", Science vol.253:164-170 (Jul. 1991).	
	A5	Brooks et al., "CHARMM: A Program for Macromolecular Energy, Minimization, and Dynamics Calculations," J. of Computational Chemistry, 4(2):187-217 (1983).	
	A6	Connolly, M.L., "Solvent-Accessible Surfaces of Proteins and Nucleic Acids", Science vol.221(4612):709-713 (Aug 1983).	
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	A10	Dahiyat, B.I., et al., "Proteins from Scratch", press digest email by Science (Sep. 26, 1997).	
	A11	Dahiyat et al., "Protein Design Automation," Meeting Abstract; Protein Science vol 4, Suppl. 2, 83 (1995).	
	A12	Dahiyat et al., "Protein design Automation," Poster Sessions, Protein Science vol.5, Suppl. 1, 22-23 (1996).	
	A13	Dahiyat et al., "De Novo Protein Design: Fully Automated Sequence Selection," Science, 278:82-87 (1997).	
	A14	Dahiyat et al., "Probing the Role of Specificity in Protein Design," Caltech Biology Annual Report, 160-161 (1996).	
	A15	Dahiyat et al., "Protein Design Automation," 1996, Protein Science, vol. 5, pp 895-903, Nov. 30, 1999.	
	A16	Dahiyat, B.I., et al., "First fully automatic design of a protein achieved by Caltech scientists", new press release (Oct. 1997).	
	A17	Dalal, S., et al., "Protein alchemy: Changing .beta.-sheet into .alpha.-helix", Nature Struc. Biol. vol.4(7):548-552 (Jul. 1997).	

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	B2	Desjarlais, J.R., et al., "De novo design of the hydrophobic cores of proteins", Protein Science 4:2006-2018 (1995).	
	B3	Desjarlais et al., "New strategies in protein design," Current Opinion in Biotechnology :460-466 (1995).	
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	B9	Goldstein, R.F., "Efficient Rotamer Elimination Applied to Protein Side-Chains and Related Spin Glasses", Biophys. Jour. vol.66:1335-1340 (May 1994).	
	B10	Gordon et al. "Energy functions for protein design," Curr. Opinion in Struct. Biol., 9:509-513 (1999).	
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	B13	Hellinga, H.W., et al., "Construction of New Ligand Binding Site in Proteins of Known Structure", J. Mol. Biol 222:763-785 (1991).	
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	B16	Holmes, "First-ever designer protein fits like a glove," New Scientist, IPC Magazines Limited, Oct. 11, 1997 (1997).	
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	C2	Koehl et al., "De Novo Protein Design I. In Search of Stability and Specificity," J. Mol. Biol., 293:1161-1181 (1999).	
	C3	Kono et al., "Energy Minimization Method Using Automata Network for Sequence and Side-Chain Conformation Prediction from Given Backbone Geometry," Proteins: Structure, Function, and Genetics, 19:244-255 (1994).	
	C4	Kortemme et al., "Design of a 20-Amino Acid, Three-Stranded β-Sheet Protein," Science, 281:253-256 (1988).	
	C5	Lasters et al., "Enhanced dead-end elimination in the search for the global minimum energy conformation of a collection of protein side chains," 1995, Protein Engineering, vol 8, No 8, pp. 815-822.	
	C6	Lasters, I., et al , "Dead-End Based Modeling Tools to Explore the Sequence Space That is Compatible with a Given Scaffold", Jour. of Protein Chem. vol.16(5):449-452 (Jul. 1997).	
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	C8	Lee et al , "Accurate prediction of the stability and activity effects of site-directed mutagenesis on a protein core," Nature, 352 448-451 (1991).	
	C9	Lim et al., "The crystal structure of a mutant protein with altered but improved hydrophobic core packing," Proc Natl Acad Sci U S A. 1994 Jan 4;91(1):423-7	
	C10	Mayo et al., "DREIDING: A Generic Force Field for Molecular Simulations," J. Phys. Chem., 94:8897-8909 (1990).	
	C11	Minor Jr., D.L., "Measurement of the .beta.-sheet-forming propensities of amino acids", Nature vol.367:660-663 (Feb. 1994).	
	C12	Munoz, V., et al., "Helix design, prediction and stability", Curr. Opin. in Biotech. 6:382-386 (Aug. 1995).	
	C12	Munoz, V., et al , "Intrinsic Secondary Structure Propensities of the Amino Acids, Using Statistical phi-psi Matrices: Comparison with Experimental Scales", Proteins 20:301-311 (1994).	
	C14	Munoz, V., et al , "Analysis of the effect of local interactions on protein stability", Folding & Design 1(3):167-178 (Apr. 1996).	
	C15	Pabo, C., "Designing proteins and peptides", Nature vol.301:200 (Jan. 1983).	
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	C17	Ponder, J.W., et al , "Use of Packing Criteria in the Enumeration of Allowed Sequences for Different Structural Classes", release by Acad Press Inc. (London) Ltd. pp.775-791(1987).	
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	D2	Smith, C.K., et al., "Guidelines for Protein Design: The Energetics of .beta. Sheet Side Chain Interactions", Science vol.270:980-982 (Nov. 1995).	
	D3	Stickle et al., "Hydrogen Bonding in Globular Proteins," (1992) Journal of Molecular Biology, vol.226, pp. 1143-1159.	
	D4	Sun, S., et al., "Designing amino acid sequences to fold with good hydrophobic cores", Protein Eng. vol.8(12):1205-1213 (1995).	
	D5	Tuffery et al., "A New Approach to the Rapid Determination of Protein Side Chain Conformations," J. of Biomolecular Struct. & Dynamics, 8(6):1267-1289 (1991).	
	D6	van Gunsteren et al., "Prediction of the Activity and Stability Effects of Site-directed Mutagenesis on a Protein Core," J. Mol. Biol., 227:389-395 (1992).	
	D7	Villegas et al., "Stabilization of proteins by rational design of .alpha.-helix stability using helix/coil transition theory," Folding & Design, 1(1):29-34 (1995).	
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